FIGURE 1

TTGGCGGGCGGAAGCGGCCACAACCCGGCGATCGAAAAGATTCTTAGGAACGCCGTACCA
GCCGCGTCTCTCAGGACAGCAGGCCCCTGTCCTTCTGTCGGGCGCCGCTCAGCCGTGCCC
TCCGCCCCTCAGGTTCTTTTTCTAATTCCAAATAAACTTGCAAGAGGACT**ATG**AAAGATT
ATGATGAACTTCTCAAATATTATGAATTACATGAAACTATTGGGACAGGTGGCTTTGCAA
AGGTCAAACTTGCCTGCCATATCCTTACTGGAGAGATGGTAGCTATAAAAATCATGGATA
AAAACACACTAGGGAGTGATTTGCCCCGGATCAAAACGGAGATTGAGGCCTTGAAGAACC
TGAGACATCAGCATATATGTCAACTCTACCATGTGCTAGAGACAGCCAACAAAATATTCA
TGGTTCTTGAGTACTGCCCTGGAGGAGAGCTGTTTGACTATATAATTTCCCAGGATCGCC
TGTCAGAAGAGGAGACCCGGGTTGTCTTCCGTCAGATAGTATCTGCTGTTGCTTATGTGC
ACAGCCAGGGCTATGCTCACAGGGACCTCAAGCCAGAAAATTTGCTGTTTGATGAATATC
ATAAATTAAAGCTGATTGACTTTGGTCTCTGTGCAAAACCCAAGGGTAACAAGGATTACC
ATCTACAGACATGCTGTGGGAGTCTGGCTTATGCAGCACCTGAGTTAATACAAGGCAAAT
CATATCTTGGATCAGAGGCAGATGTTTGGAGCATGGGCATACTGTTATATGTTCTTATGT
GTGGATTTCTACCATTTGATGATGATAATGTAATGGCTTTATACAAGAAGATTATGAGAG
GAAAATATGATGTTCCCAAGTGGCTCTCTCCCAGTAGCATTCTGCTTCTTCAACAAATGC
TGCAGGTGGACCCAAAGAAACGGATTTCTATGAAAAATCTATTGAACCATCCCTGGATCA
TGCAAGATTACAACTATCCTGTTGAGTGGCAAAGCAAGAATCCTTTTATTCACCTCGATG
ATGATTGCGTAACAGAACTTTCTGTACATCACAGAAACAACAGGCAAACAATGGAGGATT
TAATTTCACTGTGGCAGTATGATCACCTCACGGCTACCTATCTTCTGCTTCTAGCCAAGA
AGGCTCGGGGAAAACCAGTTCGTTTAAGGCTTTCTTCTTTCTCCTGTGGACAAGCCAGTG
CTACCCCATTCACAGACATCAAGTCAAATAATTGGAGTCTGGAAGATGTGACCGCAAGTG
ATAAAAATTATGTGGCGGGATTAATAGACTATGATTGGTGTGAAGATGATTTATCAACAG
GTGCTGCTACTCCCCGAACATCACAGTTTACCAAGTACTGGACAGAATCAAATGGGGTGG
AATCTAAATCATTAACTCCAGCCTTATGCAGAACACCTGCAAATAAATTAAAGAACAAAG
AAAATGTATATACTCCTAAGTCTGCTGTAAAGAATGAAGAGTACTTTATGTTTCCTGAGC
CAAAGACTCCAGTTAATAAGAACCAGCATAAGAGAGAAATACTCACTACGCCAAATCGTT
ACACTACACCCTCAAAAGCTAGAAACCAGTGCCTGAAAGAAACTCCAATTAAAATACCAG
TAAATTCAACAGGAACAGACAAGTTAATGACAGGTGTCATTAGCCCTGAGAGGCGGTGCC
GCTCAGTGGAATTGGATCTCAACCAAGCACATATGGAGGAGACTCCAAAAAGAAAGGGAG
CCAAAGTGTTTGGGAGCCTTGAAAGGGGGTTGGATAAGGTTATCACTGTGCTCACCAGGA
GCAAAAGGAAGGGTTCTGCCAGAGACGGGCCCAGAAGACTAAAGCTTCACTATAATGTGA
CTACAACTAGATTAGTGAATCCAGATCAACTGTTGAATGAAATAATGTCTATTCTTCCAA
AGAAGCATGTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAAACACAGTCAGATT
TTGGGAAAGTGACAATGCAATTTGAATTAGAAGTGTGCCAGCTTCAAAAACCCGATGTGG
TGGGTATCAGGAGGCAGCGGCTTAAGGGCGATGCCTGGGTTTACAAAAGATTAGTGGAAG
ACATCCTATCTAGCTGCAAGGTA**TAA**TTGATGGATTCTTCCATCCTGCCGGATGAGTGTG
GGTGTGATACAGCCTACATAAAGACTGTTATGATCGCTTTGATTTTAAAGTTCATTGGAA
CTACCAACTTGTTTCTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTTTAAACAAAA
GATATTATTTTGTGTATGAATCTAAATCAAGCCCATCTGTCATTATGTTACTGTCTTTTT
TAATCATGTGGTTTTGTATATTAATAATTGTTGACTTTCTTAGATTCACTTCCATATGTG
AATGTAAGCTCTTAACTATGTCTCTTTGTAATGTGTAATTTCTTTCTGAAATAAAACCAT
TTGTGAATAT

FIGURE 2

MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSDLPRIKTEIEA
LKNLRHQHICQLYHVLETANKIFMVLEYCPGGELFDYIISQDRLSEEETRVVFRQIVSAV
AYVHSQGYAHRDLKPENLLFDEYHKLKLIDFGLCAKPKGNKDYHLQTCCGSLAYAAPELI
QGKSYLGSEADVWSMGILLYVLMCGFLPFDDDNVMALYKKIMRGKYDVPKWLSPSSILLL
QQMLQVDPKKRISMKNLLNHPWIMQDYNYPVEWQSKNPFIHLDDDCVTELSVHHRNNRQT
MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSFSCGQASATPFTDIKSNNWSLEDV
TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALCRTPANKL
KNKENVYTPKSAVKNEEYFMFPEPKTPVNKNQHKREILTTPNRYTTPSKARNQCLKETPI
KIPVNSTGTDKLMTGVISPERRCRSVELDLNQAHMEETPKRKGAKVFGSLERGLDKVITV
LTRSKRKGSARDGPRRLKLHYNVTTTRLVNPDQLLNEIMSILPKKHVDFVQKGYTLKCQT
QSDFGKVTMQFELEVCQLQKPDVVGIRRQRLKGDAWVYKRLVEDILSSCKV

N-glycosylation site.

354-357
485-488
562-565

cAMP- and cGMP-dependent protein kinase phosphorylation site.

250-253
546-549

Tyrosine kinase phosphorylation site.

2-10
421-427
630-638

N-myristoylation site.

340-345

Microbodies C-terminal targeting signal.

649-652

Leucine zipper pattern.

165-186

Serine/Threonine protein kinases active-site signature.

128-140

Protein kinase domain

11-263

Kinase associated domain 1

602-651

FIGURE 3

GTGCGATCCCGGGCCCGAGGGCATCAGACGGCGGCTGATTAGCTCCGGTTTGCATCACCC
GGACCGGGGGATTAGCTCCGGTTTGCATCACCCGGACCGGGGGCCGGGCGCGCACGAGAC
TCGCAGCGGAAGTGGAGGCGGCTCCGCGCGCGTCCGCTGCTAGGACCCGGGCAGGGCTGG
AGCTGGGCTGGGATCCCGAGCTCGGCAGCAGCGCAGCGGGCCGGCCCACCTGCTGGTGCC
CTGGAGGCTCTGAGCCCCGGCGGCGCCCGGGCCCACGCGGAACGACGGGGCGAG**ATG**CGA
GCCACCCCTCTAGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAGTTGGAT
GACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGCCCAGA
CTGCCCCCCTGCCTGTTGCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTG
GCCACTGCCTCCCGTCTTGGGCCCTATGTCCTCCTGGAGCCCGAGGAGGGCGGGCGGGCC
TACCAGGCCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCCGTCCAG
GAAGCCCCGGCCGTGCTGGAGCCCTATGCGCGGCTGCCCCCGCACAAGCATGTGGCTCGG
CCCACTGAGGTCCTGGCTGGTACCCAGCTCCTCTACGCCTTTTTCACTCGGACCCATGGG
GACATGCACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGCCTGAGGCTGCCGTGCTC
TTCCGCCAGATGGCCACCGCCCTGGCGCACTGTCACCAGCACGGTCTGGTCCTGCGTGAT
CTCAAGCTGTGTCGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTGGTGCTGGAGAAC
CTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCACGCGTGC
CCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAGGCAGCC
GATGTCTGGAGCCTGGGCGTGGCGCTCTTCACCATGCTGGCCGGCCACTACCCCTTCCAG
GACTCGGAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCGGGGCCTACGCCTTGCCTGCA
GGCCTCTCGGCCCCTGCCCGCTGTCTGGTTCGCTGCCTCCTTCGTCGGGAGCCAGCTGAA
CGGCTCACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGATGCCCTTA
GCCCCAACCCGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGATGGTCTGGGGCTG
GACGAAGCCAGGGAAGAGGAGGGAGACAGAGAAGTGGTTCTGTATGGC**TAG**GACCACCCT
ACTACACGCTCAGCTGCCAACAGTGGATTGAGTTTGGGGGTAGCTCCAAGCCTTCTCCTG
CCTCTGAACTGAGCCAAACCTTCAGTGCCTTCCAGAAGGGAGAAAGGCAGAAGCCTGTGT
GGAGTGTGCTGTGTACACATCTGCTTTGTTCCACACACATGCAGTTCCTGCTTGGGTGCT
TATCAGGTGCCAAGCCCTGTTCTCGGTGCTGGGAGTACAGCAGTGAGCAAAGGAGACAAT
ATTCCCTGCTCACAGAGATGACAAACTGGCATCCTTGAGCTGACAACACTTTTCCATGAC
CATAGGTCACTGTCTACACTGGGTACACTTTGTACCAGTGTCGGCCTCCACTGATGCTGG
TGCTCAGGCACCTCTGTCCAAGGACAATCCCTTTCACAAACAAACCAGCTGCCTTTGTAT
CTTGTACCTTTTCAGAGAAAGGGAGGTATCCCTGTGCCAAAGGCTCCAGGCCTCTCCCCT
GCAACTCAGGACCCAAGCCCAGCTCACTCTGGGAACTGTGTTCCCAGCATCTCTGTCCTC
TTGATTAAGAGATTCTCCTTCCAGGCCTAAGCCTGGGATTTGGGCCAGAGATAAGAATCC
AAACTATGAGGCTAGTTCTTGTCTAACTCAAGACTGTTCTGGAATGAGGGTCCAGGCCTG
TCAACCATGGGGCTTCTGACCTGAGCACCAAGGTTGAGGGACAGGATTAGGCAGGGTCTG
TCCTGTGGCCACCTGGAAAGTCCCAGGTGGGACTCTTCTGGGGACACTTGGGGTCCACAA
TCCCAGGTCCATACTCTAGGTTTTGGATACCATGAGTATGTATGTTTACCTGTGCCTAAT
AAAGGAGAATTATGAAATAAAAAAAAAAAAAAAAAA

FIGURE 4

MRATPLAAPAGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPPTAPDRAT
AVATASRLGPYVLLEPEEGGRAYQALHCPTGTEYTCKVYPVQEAPAVLEPYARLPPHKHV
ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVL
RDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGK
AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP
AERLTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG

N-myristoylation site.

91-96
341-346

Protein kinase domain

71-315

FIGURE 5

GAAGTTTCTCACTAGGGTCTTCTCTGGCCCAGCCTTTGACTGAAGCTGGTCTGGAGACAG
GGGCATTAGAGAAGTGACTCATAGATGGCCTAAAGAAGCGGGGCCACTCAAGGACCCAGG
ACAGAGGGAAGAGGGCCAACCCAGCTGGACCACAGGCAAACCCCATTGCCTTTGAGAGAA
AGAAGAGGACCCGGTGAAAC**ATG**CTGCTGCTGAAGAAACACACGGAGGACATCAGCAGCG
TCTACGAGATCCGCGAGAGGCTCGGCTCGGGTGCCTTCTCCGAGGTGGTGCTGGCCCAGG
AGCGGGGCTCCGCACACCTCGTGGCCCTCAAGTGCATCCCCAAGAAGGCCCTCCGGGGCA
AGGAGGCCCTGGTGGAGAACGAGATCGCAGTGCTCCGTAGGATCAGTCACCCCAACATCG
TCGCTCTGGAGGATGTCCACGAGAGCCCTTCCCACCTCTACCTGGCCATGGAACTGGTGA
CGGGTGGCGAGCTGTTTGACCGCATCATGGAGCGCGGCTCCTACACAGAGAAGGATGCCA
GCCATCTGGTGGGTCAGGTCCTTGGCGCCGTCTCCTACCTGCACAGCCTGGGGATCGTGC
ACCGGGACCTCAAGCCCGAAAACCTCCTGTATGCCACGCCCTTTGAGGACTCGAAGATCA
TGGTCTCTGACTTTGGACTCTCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTG
GGACCCCTGGATATGTGGCCCCAGAGCTCTTGGAGCAGAAACCCTACGGGAAGGCCGTAG
ATGTGTGGGCCCTGGGCGTCATCTCCTACATCCTGCTGTGTGGGTACCCCCCCTTCTACG
ACGAGAGCGACCCTGAGCTCTTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTXTC
CTTTCTGGGATGACATCTCAGAATCAGGCAAAGACTTTATTCGGCACCTTCTGGAGCGAG
ACCTTCAGAAGAGGTTCACCTGCCAACAGGCCTTGCGGGACCTTTGGATCTTTTGGGACA
CAGGCTTTGGCAGGGACATCTTAGGGTTTGTCAGTGAGCAGATCCGGAAGAACTTTGCTT
GGACACACTGGAAGCGAGCCTTCAATGCCACCTTGTTCCTGCGCCACATCCGGAAGCTGG
GGCAGATCCCAGAGGGCGAGGGGGCCTCTGAGCAGGGCATGGSCCGXCACAGCCACTXAG
GCCTTCGTGCTGGCCAGCCCCCCAAGTGG**TGA**TGCCCAGGXAGATGCCGAGGCCAAGTGG
AXTGAXCCCCAGATTTXCTTXC

FIGURE 6

MLLLKKHTEDISSVYEIRERLGSGAFSEVVLAQERGSAHLVALKCIPKKALRGKEALVEN
EIAVLRRISHPNIVALEDVHESPSHLYLAMELVTGGELFDRIMERGSYTEKDASHLVGQV
LGAVSYLHSLGIVHRDLKPENLLYATPFEDSKIMVSDFGLSKIQAGNMLGTACGTPGYVA
PELLEQKPYGKAVDVWALGVISYILLCGYPPFYDESDPELFSQILRASYEFDXPFWDDIS
ESGKDFIRHLLERDLQKRFTCQQALRDLWIFWDTGFGRDILGFVSEQIRKNFAWTHWKRA
FNATLFLRHIRKLGQIPEGEGASEQGMXRHSHXGLRAGQPPKW

N-glycosylation site.

302-305

cAMP- and cGMP-dependent protein kinase phosphorylation site.

5-8
66-69
257-260

Tyrosine kinase phosphorylation site.

101-108

N-myristoylation site.

118-123
166-171
170-175
334-339

Serine/Threonine protein kinases active-site signature.

132-144

Protein kinase domain

15-270

FIGURE 7

TASK110 expression data

Tumor samples versus cell lines

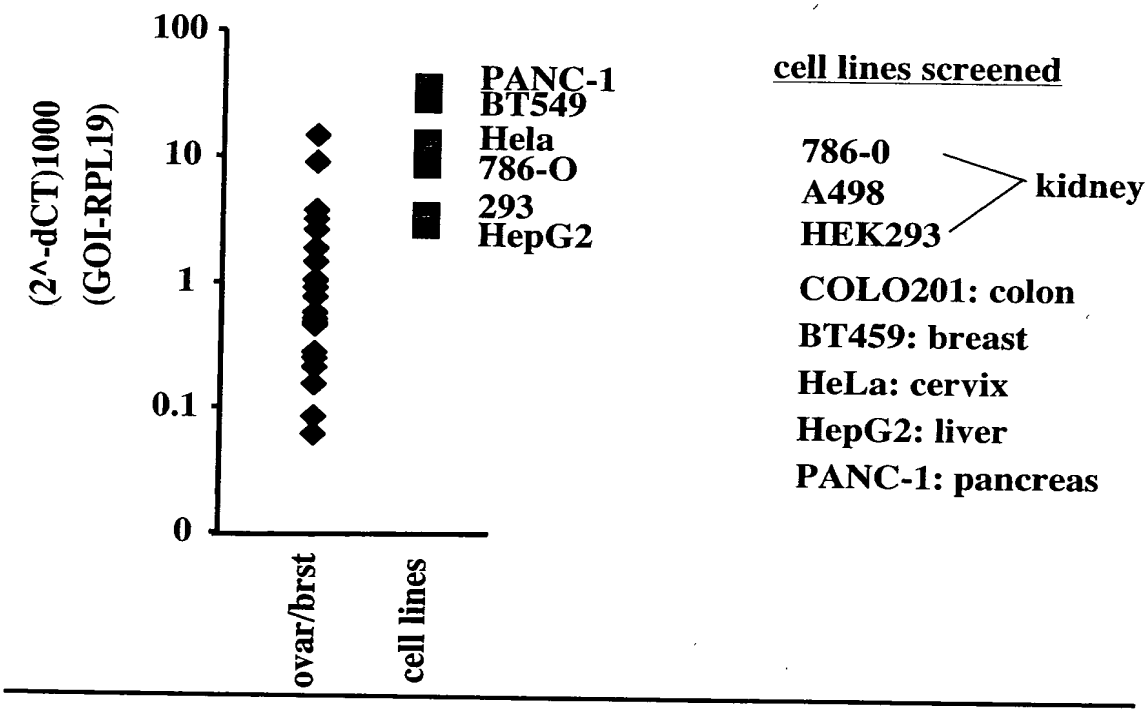


FIGURE 8

TASK119 expression: tumor samples versus cell lines

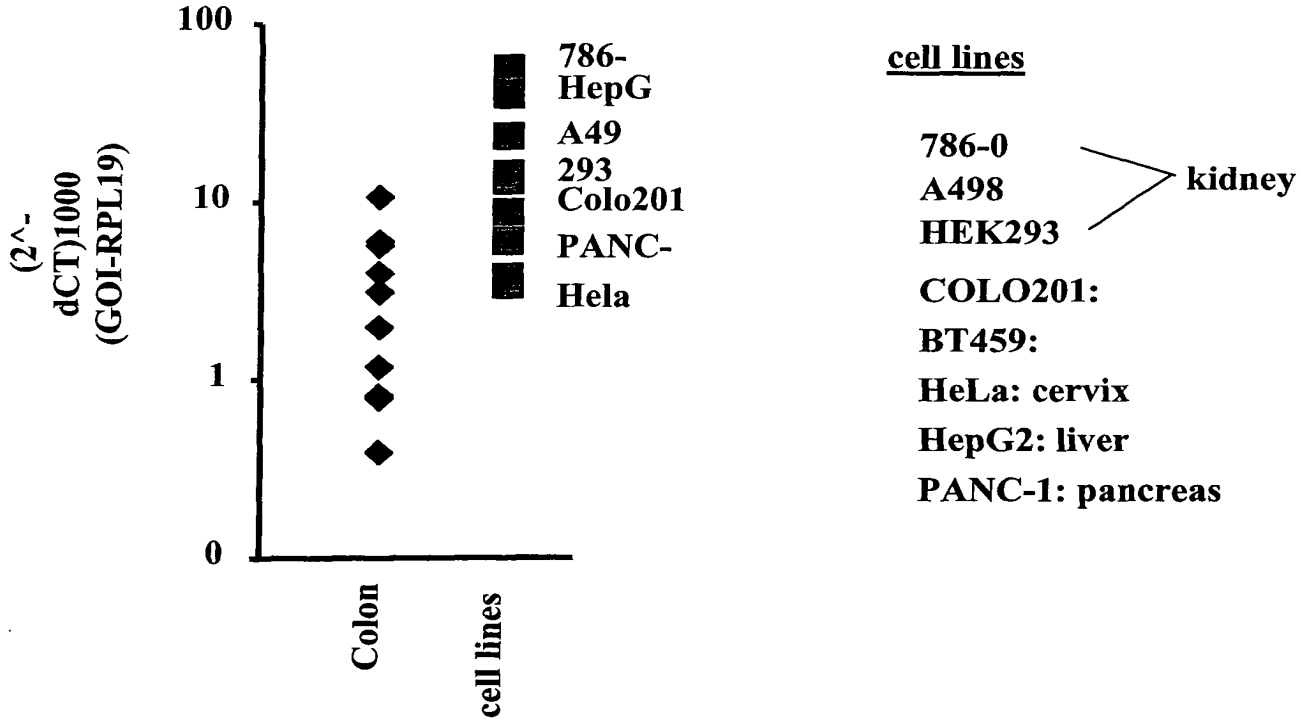


FIGURE 9A

Lung cancer in situ

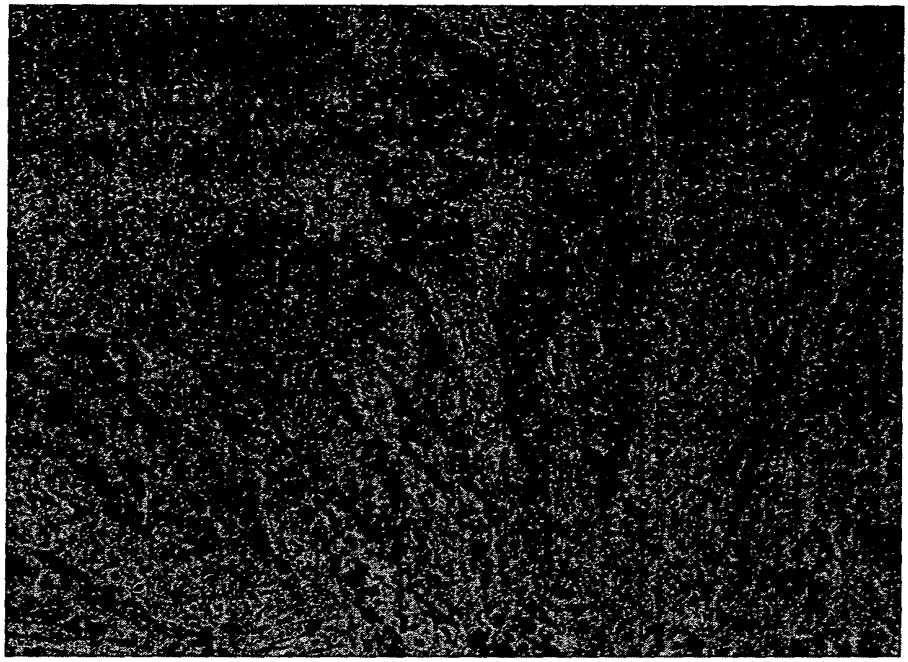


FIGURE 9B

Lung cancer in situ

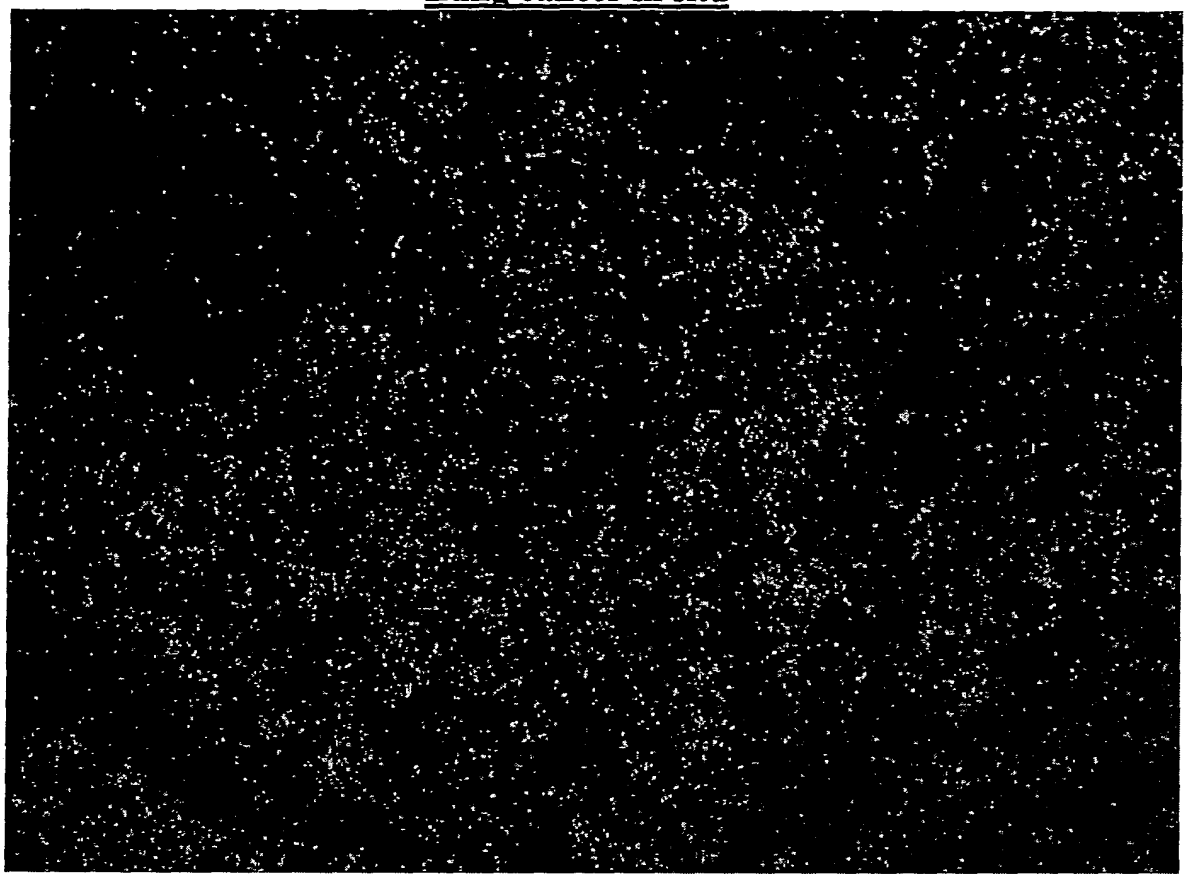


FIGURE 10A

Kidney cancer in situ

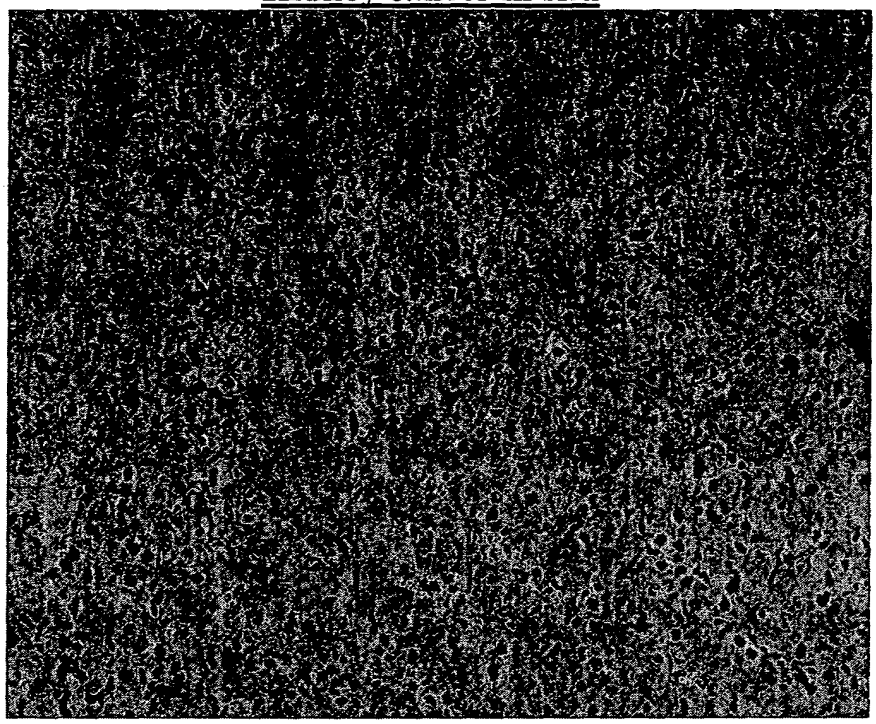


FIGURE 10B

Kidney cancer in situ

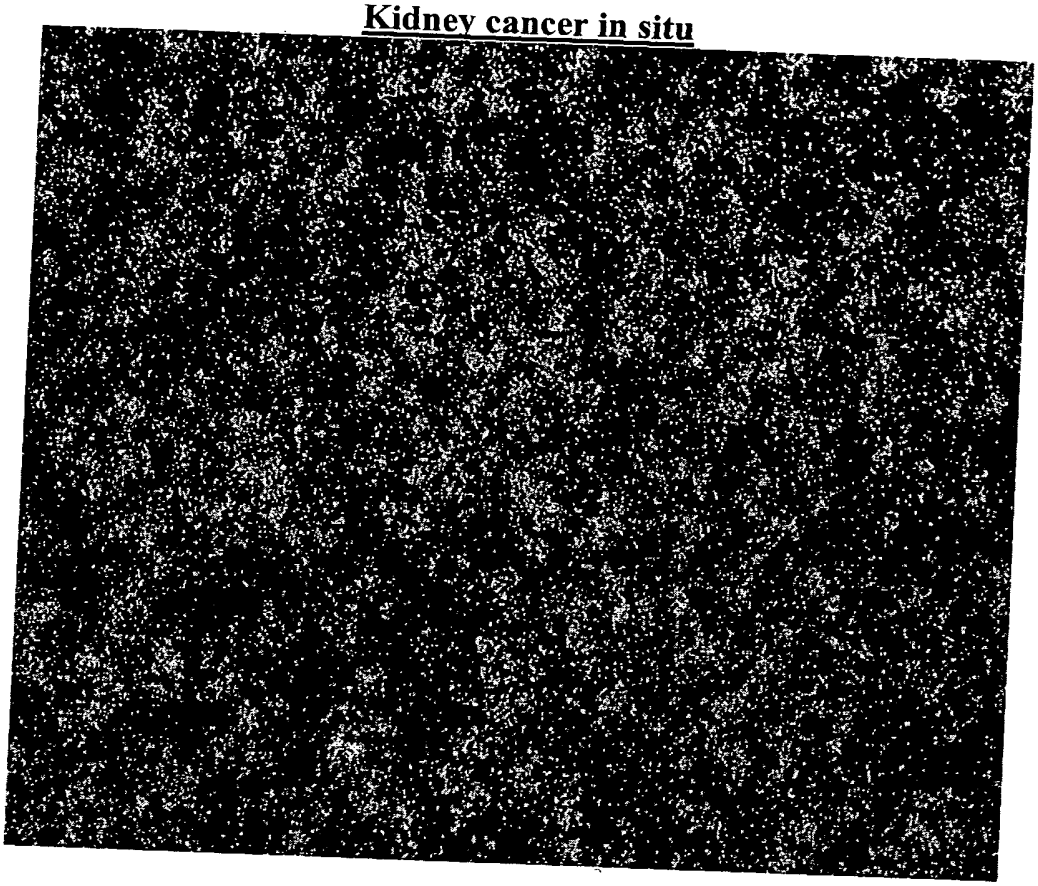


FIGURE 11A

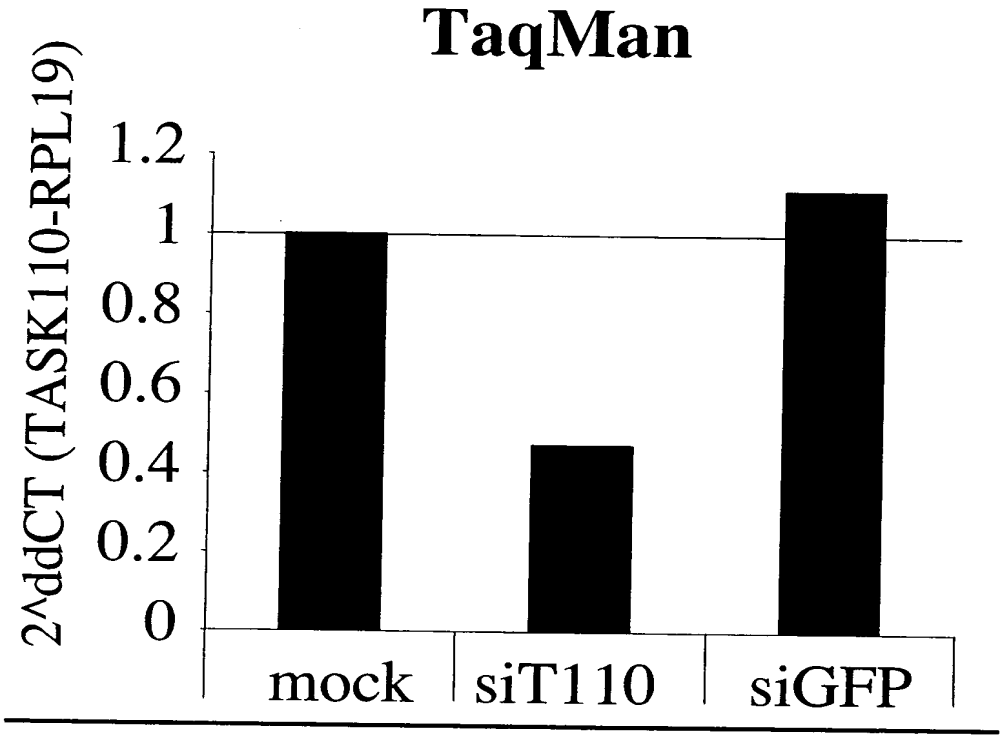

TaqMan
2^ddCT (TASK110-RPL19)
1.2
1
0.8
0.6
0.4
0.2
0
mock
siT110
siGFP

FIGURE 11B

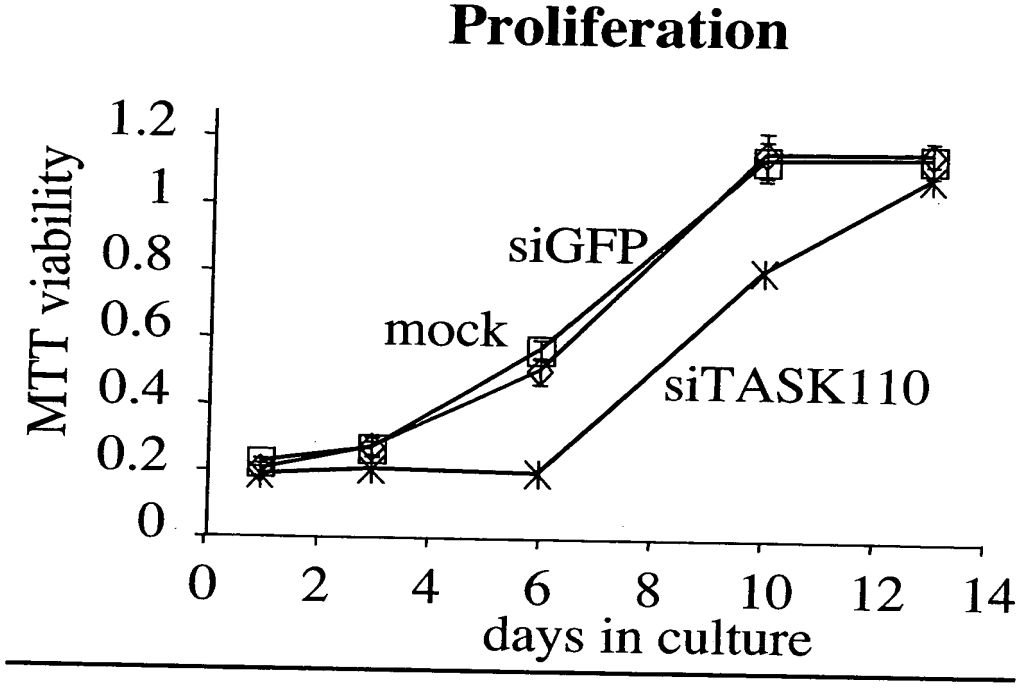

Proliferation
MTT viability
1.2
1
0.8
0.6
0.4
0.2
0
siGFP
mock
siTASK110
0
2
4
6
8
10
12
14
days in culture

FIGURE 11C

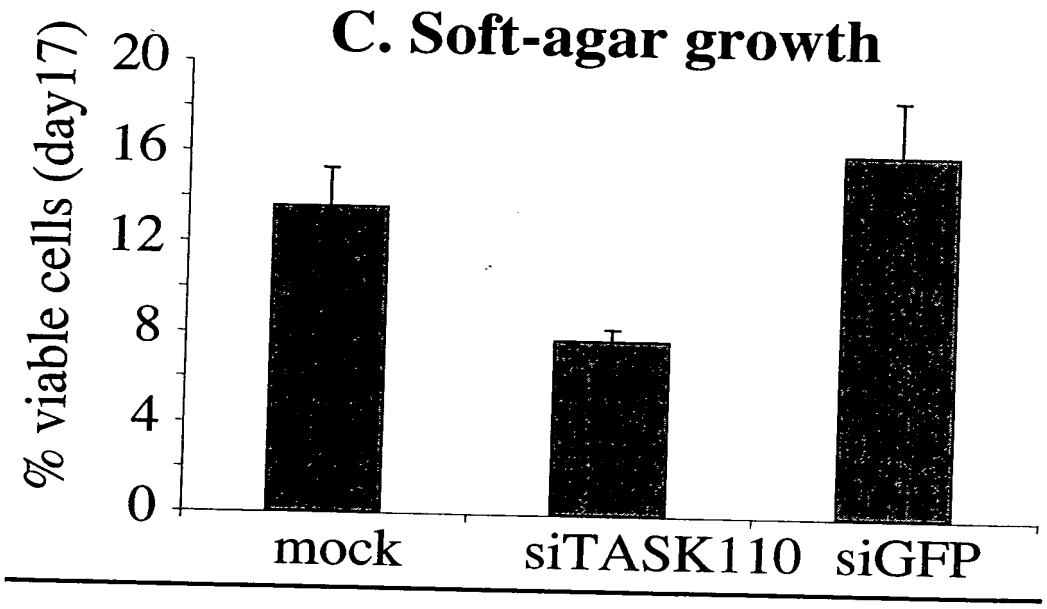

C. Soft-agar growth
% viable cells (day17)
20
16
12
8
4
0
mock
siTASK110
siGFP

FIGURE 11D

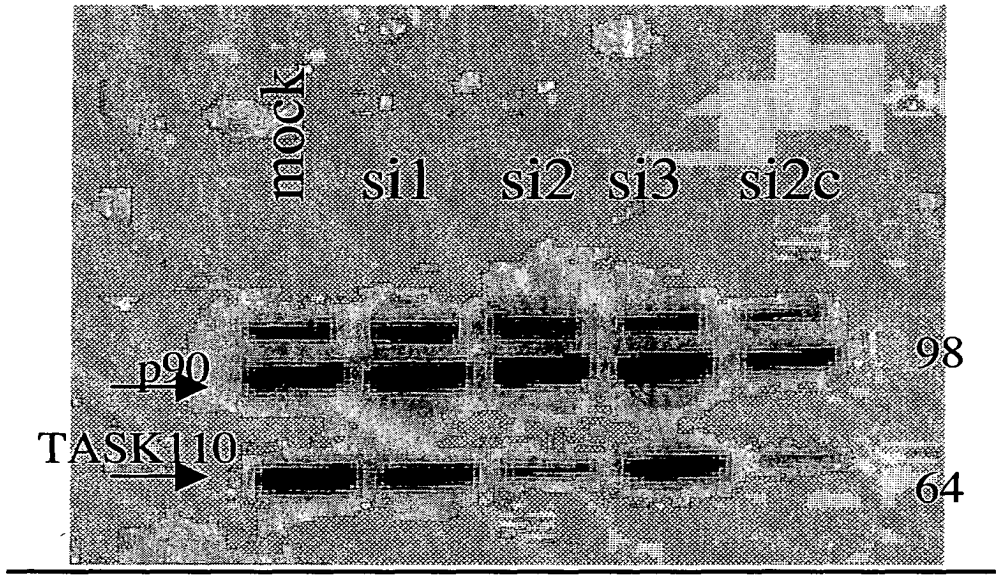


FIGURE 11E

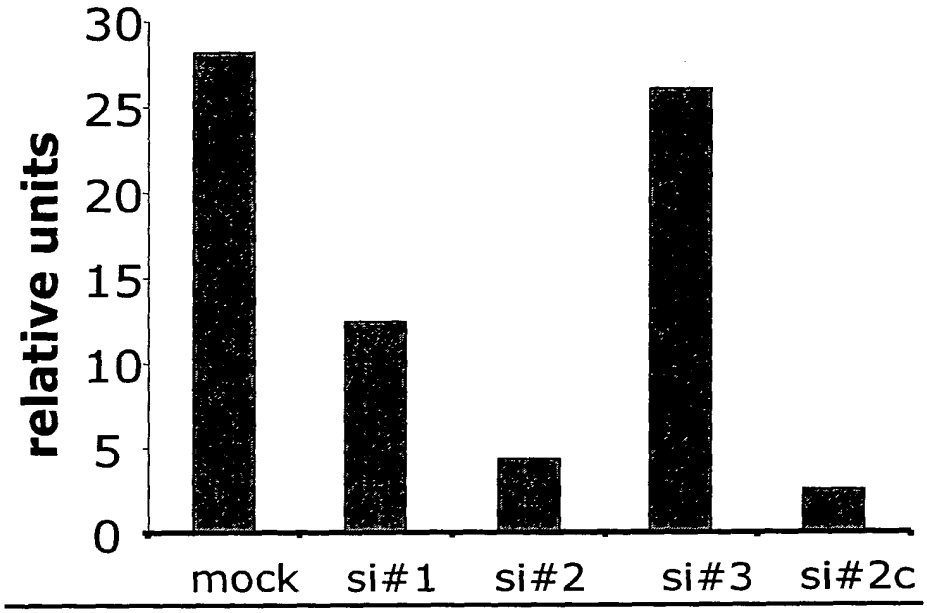


FIGURE 11F

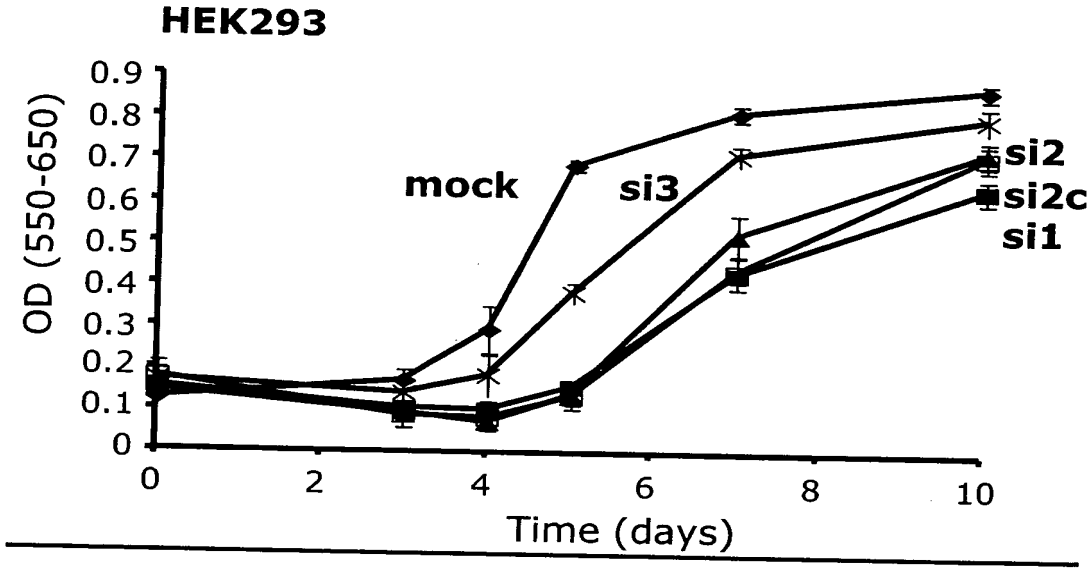

HEK293
OD (550-650)
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
2
4
6
8
10
Time (days)
mock
si3
si2
si2c
si1

FIGURE 11G

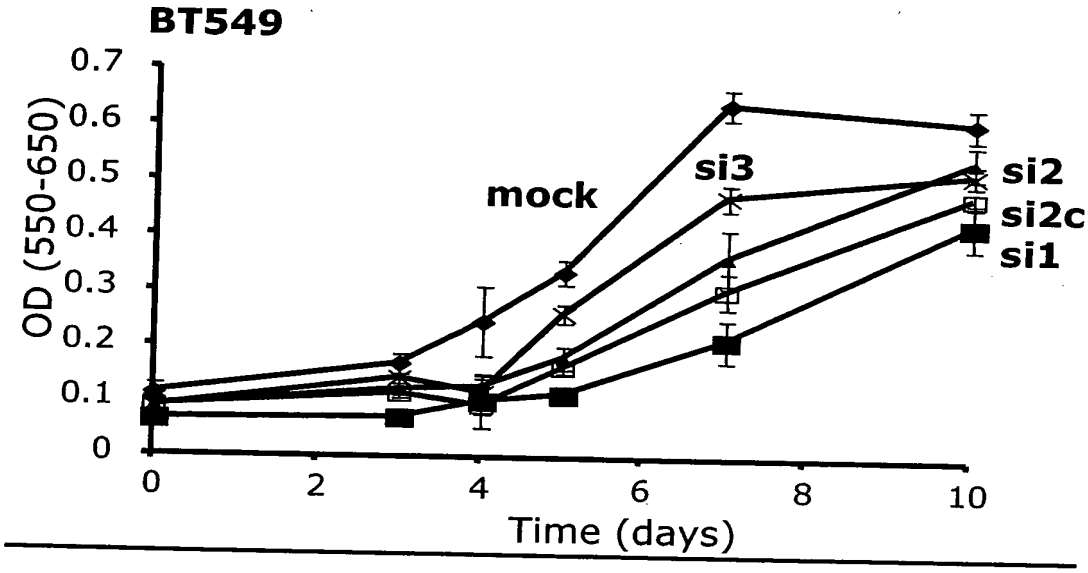

BT549
OD (550-650)
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
2
4
6
8
10
Time (days)
mock
si3
si2
si2c
si1

FIGURE 11H

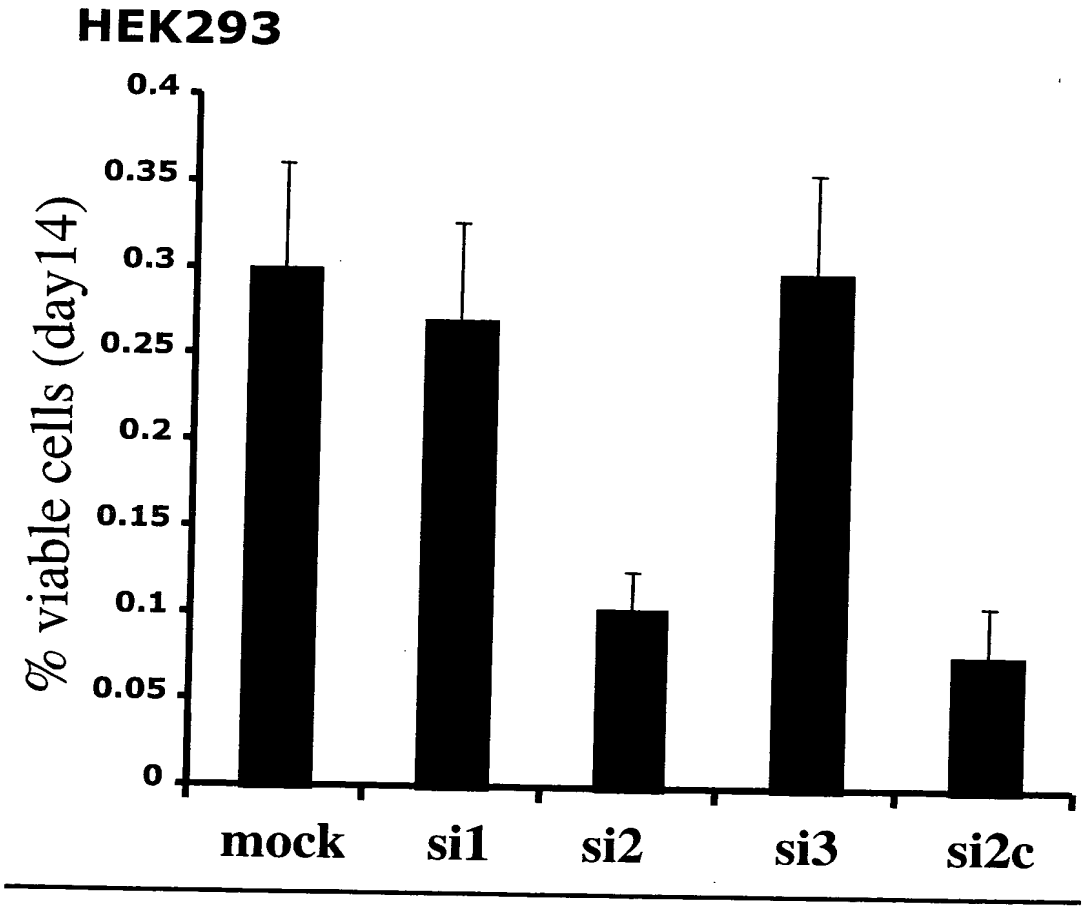

HEK293
% viable cells (day14)
0.4
0.35
0.3
0.25
0.2
0.15
0.1
0.05
0
mock
si1
si2
si3
si2c

FIGURE 11(I)

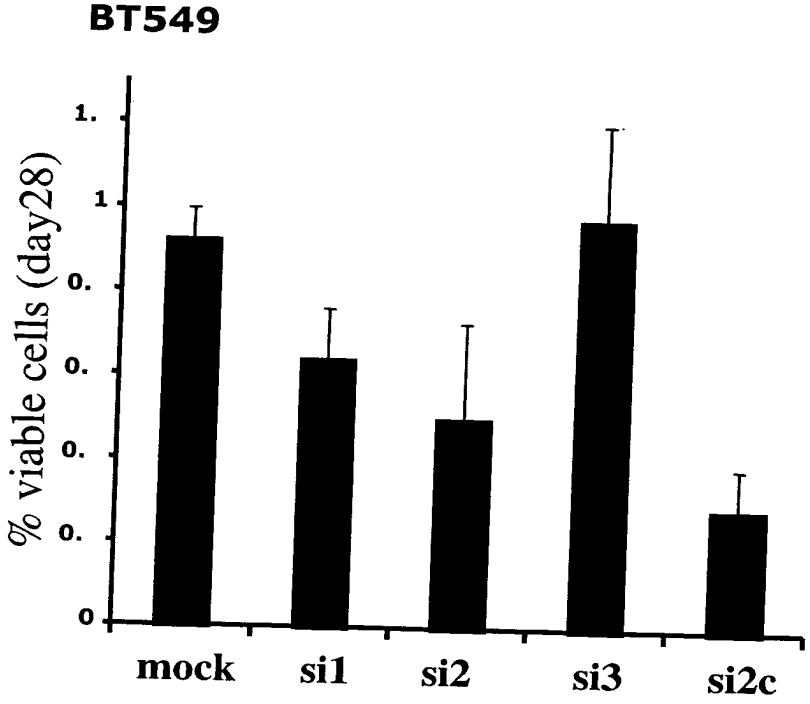


FIGURE 12

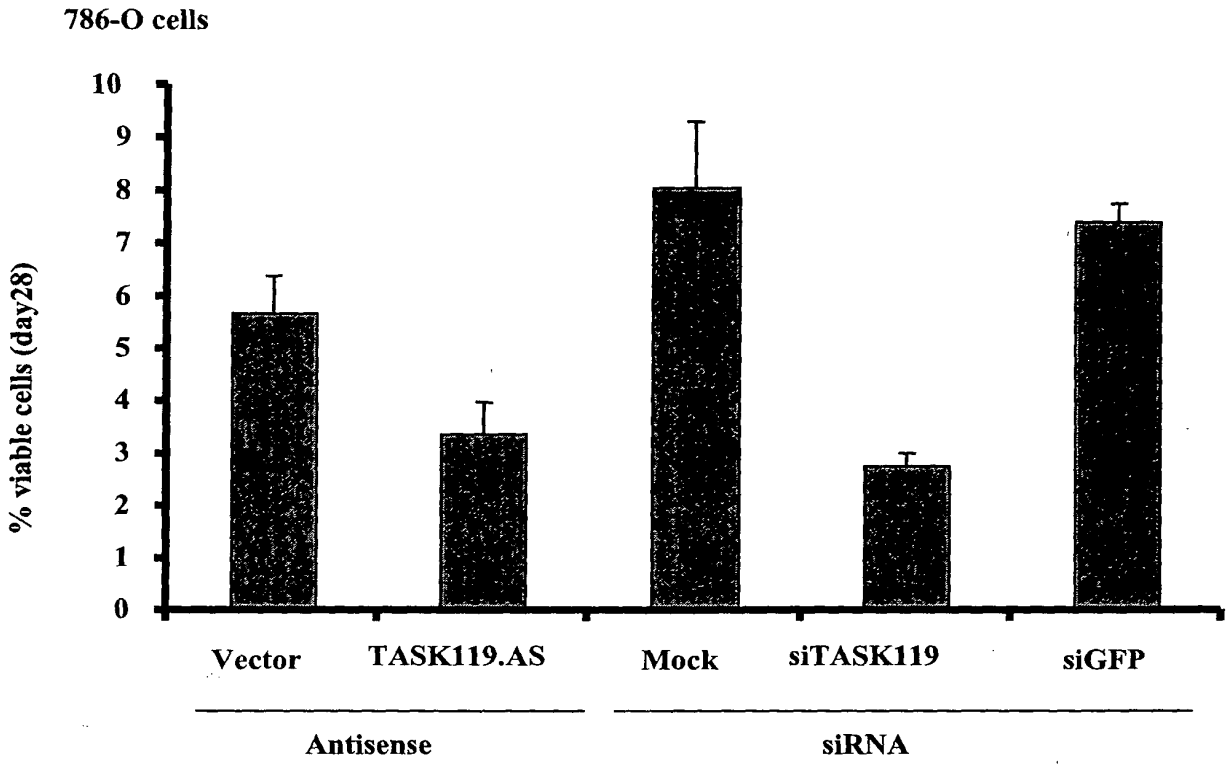
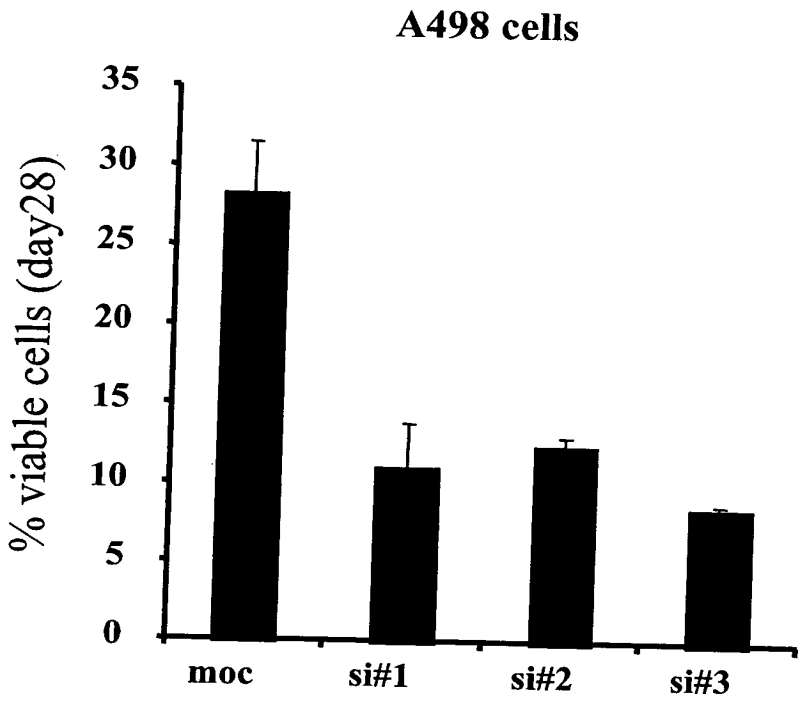
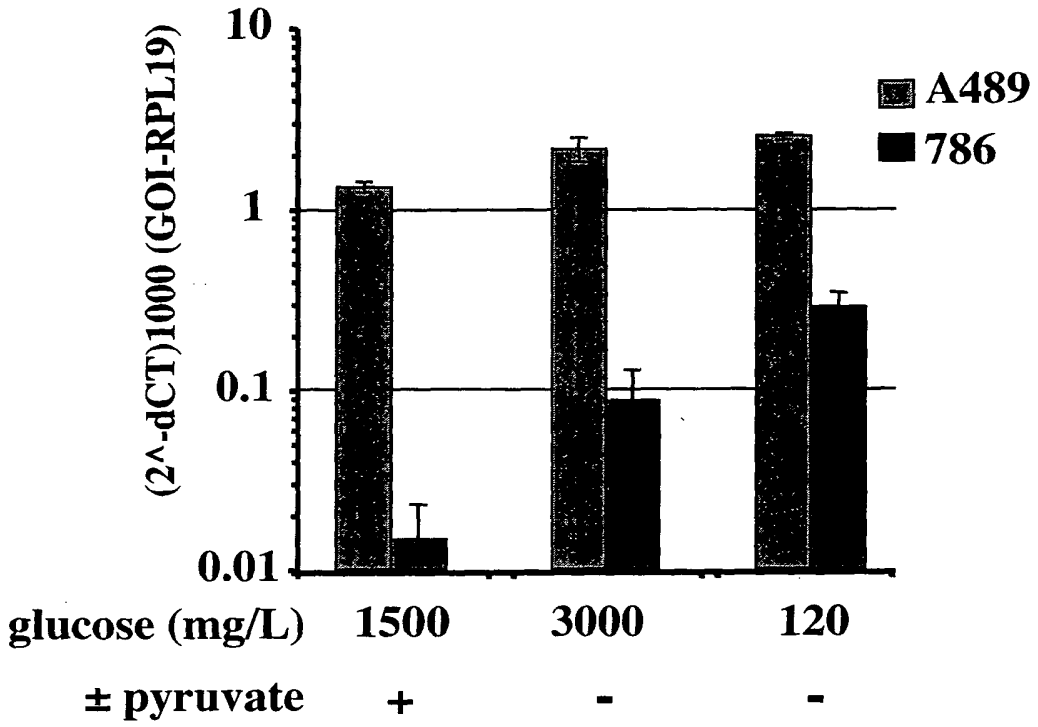

786-O cells
% viable cells (day28)
10
9
8
7
6
5
4
3
2
1
0
Vector
TASK119.AS
Mock
siTASK119
siGFP
Antisense
siRNA

FIGURE 13


A498 cells
% viable cells (day28)
35
30
25
20
15
10
5
0
moc
si#1
si#2
si#3

› 4 control genes

FIGURE 15


10
1
0.1
0.01
(2^-dCT)1000 (GOI-RPL19)
A489
786
glucose (mg/L)
1500
3000
120
± pyruvate
+
-
-